

## SEQUENCE LISTING



<110> Dattwyler, Raymond J.  
Seinost, Gerald  
Dykhuisen, Danial  
Luft, Benjamin J.  
Maria J.C. Gomes-Solecki

<120> Groups of Borrelia burgdorferi and  
Borrelia afzelii That Cause Lyme Disease in Humans

<130> 2631.1002-001

<150> US 60/140,042

<151> 1999-06-18

<160> 84

<170> FastSEQ for Windows Version 4.0

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26

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AI  
Comit

46  
2/102

<220>  
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22

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gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60  
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80  
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95  
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys  
100 105 110  
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125  
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432  
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140  
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160  
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165 170 175

47  
3/102

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat gga tcc  
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180 185 190

573

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35 40 45  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125  
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160  
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<220>  
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gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30

48  
4/102

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Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192  
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
50 55 60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240  
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
65 70 75 80

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288  
Leu Ser Gly Ala Tyr 85 Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn 95

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336  
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
100 105 110

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384  
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
115 120 125

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa 432  
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
130 135 140

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480  
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
145 150 155 160

aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528  
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
165 170 175

gct gtt aaa gag ctt aca agt cct att gt 557  
Ala Val Lys Glu Leu Thr Ser Pro Ile  
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<213> Borrelia burgdorferi

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35 40 45  
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
65 70 75 80  
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
85 90 95

Al  
Cm.t

49  
5/102

Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
100 105 110  
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
115 120 125  
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
130 135 140  
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
145 150 155 160  
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
165 170 175  
Ala Val Lys Glu Leu Thr Ser Pro Ile  
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<220>  
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Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
20 25 30  
aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct 144  
Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala  
35 40 45  
gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att gct gct 192  
Val Lys Glu Val Glu Ala Leu Ser Ser Ile Asp Glu Ile Ala Ala  
50 55 60  
aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat acc gaa 240  
Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu  
65 70 75 80  
aat aat cac aat gga tca ttg tta gcg gga gct tat gca ata tca acc 288  
Asn Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr  
85 90 95  
cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta aag gaa 336  
Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu  
100 105 110  
aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat aaa tta 384  
Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu  
115 120 125  
aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat gct gat 432  
Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp  
130 135 140

AI  
Cm.t

50  
~~6/102~~

gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa ggt gct	480
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145 150 155 160	
gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca aaa gca	528
Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala	
165 170 175	
gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc cct gtt	576
Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val	
180 185 190	
gtg	579
Val	

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 <212> PRT  
 <213> Borrelia burgdorferi

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20 25 30	
Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala	
35 40 45	
Val Lys Glu Val Glu Ala Leu Ser Ser Ile Asp Glu Ile Ala Ala	
50 55 60	
Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu	
65 70 75 80	
Asn Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr	
85 90 95	
Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu	
100 105 110	
Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu	
115 120 125	
Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp	
130 135 140	
Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala	
145 150 155 160	
Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala	
165 170 175	
Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val	
180 185 190	
Val	

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AI  
 Cm.f

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1 5 10 15

aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96  
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
20 25 30

aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct 144  
Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala  
35 40 45

gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt gct aaa 192  
Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys  
50 55 60

gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat gaa gca 240  
Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala  
65 70 75 80

aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca acc tta 288  
Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu  
85 90 95

ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta aag gaa 336  
Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu  
100 105 110

aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act aaa cta 384  
Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu  
115 120 125

aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat gaa aat 432  
Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn  
130 135 140

gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat aag ggc 480  
Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly  
145 150 155 160

gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta tca aaa 528  
Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys  
165 170 175

gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc cct 576  
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro  
180 185 190

gtt gtg 582  
Val Val

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52  
-8/102

<213> Borrelia brgdorferi

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Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala  
35 40 45  
Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys  
50 55 60  
Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala  
65 70 75 80  
Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu  
85 90 95  
Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu  
100 105 110  
Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu  
115 120 125  
Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn  
130 135 140  
Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly  
145 150 155 160  
Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys  
165 170 175  
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro  
180 185 190  
Val Val

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<213> Borrelia burgdorferi

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<221> CDS

<222> (1)...(576)

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1 5 10 15  
aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96  
Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
20 25 30  
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144  
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
35 40 45  
gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc 192  
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
50 55 60



53  
-9/102

aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc aat cag 240  
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln  
65 70 75 80

agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta 288  
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu  
85 90 95

ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag 336  
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys  
100 105 110

att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa 384  
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys  
115 120 125

agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca 432  
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala  
130 135 140

caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca 480  
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala  
145 150 155 160

gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct 528  
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala  
165 170 175

caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576  
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val  
180 185 190

<210> 14  
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<213> Borrelia burgdorferi

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Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
35 40 45  
Val Lys Glu Val Glu Thr Leu Ala Ser Ile Asp Glu Leu Ala Thr  
50 55 60  
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln  
65 70 75 80  
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu  
85 90 95  
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys  
100 105 110  
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys  
115 120 125  
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala  
130 135 140

AI  
Con.t

54  
10/102

Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala  
145 150 155 160  
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala  
165 170 175  
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val  
180 185 190

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1 5 10 15  
aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt 96  
Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
20 25 30  
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144  
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
35 40 45  
gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc 192  
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
50 55 60  
aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag 240  
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln  
65 70 75 80  
agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta 288  
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu  
85 90 95  
ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag 336  
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys  
100 105 110  
att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa 384  
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys  
115 120 125  
agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca 432  
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala  
130 135 140  
caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca 480  
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala  
145 150 155 160

55  
11/102

gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct 528  
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala  
165 170 175

caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576  
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val  
180 185 190

<210> 16  
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<212> PRT  
<213> borrelia burgdorferi

<400> 16  
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Arg Lys Asp Gly  
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Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
35 40 45  
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
50 55 60  
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln  
65 70 75 80  
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu  
85 90 95  
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys  
100 105 110  
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys  
115 120 125  
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala  
130 135 140  
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala  
145 150 155 160  
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165 170 175  
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val  
180 185 190

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<213> Borrelia burgdorferi

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<222> (1) ... (573)

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Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly  
1 5 10 15  
aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96  
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
20 25 30

AI  
cm.t

aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc	144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala	
35 40 45	
gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa	192
Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys	
50 55 60	
gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca	240
Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala	
65 70 75 80	
gat cac aac gga tca tta ata tca gga gca tat tta att tca aac tta	288
Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu	
85 90 95	
ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca	336
Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala	
100 105 110	
gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta	384
Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu	
115 120 125	
aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat	432
Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn	
130 135 140	
gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc gct	480
Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala	
145 150 155 160	
gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca	528
Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala	
165 170 175	
gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc cct	573
Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro	
180 185 190	

<210> 18  
<211> 191  
<212> PRT  
<213> Borrelia burgdorferi

<400> 18

Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly	
1 5 10 15	
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu	
20 25 30	
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala	
35 40 45	
Val Lys Glu Val Glu Thr Leu Thr Ser Ile Asp Glu Leu Ala Lys	
50 55 60	
Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala	
65 70 75 80	

AI  
Com't

57  
13/102

Asp	His	Asn	Gly	Ser	Leu	Ile	Ser	Gly	Ala	Tyr	Leu	Ile	Ser	Asn	Leu
				85					90					95	
Ile	Thr	Lys	Lys	Ile	Ser	Ala	Ile	Lys	Asp	Ser	Gly	Glu	Leu	Lys	Ala
			100					105					110		
Glu	Ile	Glu	Lys	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Ala	Lys	Leu
			115				120					125			
Lys	Gly	Glu	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Asp	Asn
			130			135					140				
Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr	Asn	Asn	Asp	Lys	Thr	Lys	Gly	Ala
					150					155					160
Asp	Glu	Leu	Glu	Lys	Leu	Phe	Glu	Ser	Val	Lys	Asn	Leu	Ser	Lys	Ala
				165					170					175	
Ala	Lys	Glu	Met	Leu	Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	
			180					185					190		

<210> 19  
 <211> 553  
 <212> DNA  
 <213> Borrelia burgdorferi

<220>  
 <221> CDS  
 <222> (1)...(553)

<400> 19																
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Met	Thr	Leu	Phe	Leu	Phe	Ile	Ser	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	
1				5					10					15		
aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt															96	
Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	
			20					25					30			
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct															144	
Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	
			35			40					45					
gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act															192	
Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr	
		50				55				60						
aaa gct att ggt aaa aaa ata gat aac aat gct ggt ttg ggt gct gaa															240	
Lys	Ala	Ile	Gly	Lys	Lys	Ile	Asp	Asn	Asn	Ala	Gly	Leu	Gly	Ala	Glu	
		65			70				75					80		
gtg ggt caa aac gga tca ttg cta gca gga gct tat gca atc tca act															288	
Val	Gly	Gln	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	
				85				90					95			
gta ata ata gaa aaa ttg agc aca tta aaa aat gta gaa gaa tta aaa															336	
Val	Ile	Ile	Glu	Lys	Leu	Ser	Thr	Leu	Lys	Asn	Val	Glu	Glu	Leu	Lys	
			100					105					110			
gaa aaa att aca aag gct aag gat tgt tct gaa aaa ttc act aaa aaa															384	
Glu	Lys	Ile	Thr	Lys	Ala	Lys	Asp	Cys	Ser	Glu	Lys	Phe	Thr	Lys	Lys	
			115				120					125				

Alt  
cm

58  
14/102

tta aaa gat agc cgc gca gag ctt ggt aaa aaa gat gcc agt gat gat	432
Leu Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp	
130 135 140	
gat gca aaa aaa gct att tta aaa aca aat caa gct aac gat aag ggt	480
Asp Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly	
145 150 155 160	
gct aaa gaa ctt aaa gag tta ttt gaa gca gta gaa agc ttg tca aaa	528
Ala Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys	
165 170 175	
gcg gct aaa gag atg cta aac aag t	553
Ala Ala Lys Glu Met Leu Asn Lys	
180	

Al  
emit

<210> 20  
<211> 184  
<212> PRT  
<213> Borrelia burgdorferi

<400> 20
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
1 5 10 15
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
35 40 45
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
50 55 60
Lys Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu
65 70 75 80
Val Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
85 90 95
Val Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys
100 105 110
Glu Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys
115 120 125
Leu Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp
130 135 140
Asp Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly
145 150 155 160
Ala Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys
165 170 175
Ala Ala Lys Glu Met Leu Asn Lys
180

<210> 21  
<211> 582  
<212> DNA  
<213> Borrelia burgdorferi

<220>  
<221> CDS  
<222> (1)...(582)

<400> 21

59  
15/102

atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg	48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly	
1 5 10 15	
aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt	96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu	
20 25 30	
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct	144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala	
35 40 45	
gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act	192
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr	
50 55 60	
aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa	240
Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu	
65 70 75 80	
gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca aaa	288
Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys	
85 90 95	
cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag	336
Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys	
100 105 110	
gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa	384
Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys	
115 120 125	
cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat gag	432
Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu	
130 135 140	
aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag ggc	480
Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly	
145 150 155 160	
gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa	528
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys	
165 170 175	
gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agt cct	576
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro	
180 185 190	
att gtg	582
Ile Val	

<210> 22  
 <211> 194  
 <212> PRT  
 <213> Borrelia burgdorferi  
 <400> 22

Al  
Cm.t

60  
16/102

Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly  
1 5 10 15  
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
20 25 30  
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
35 40 45  
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
50 55 60  
Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu  
65 70 75 80  
Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys  
85 90 95  
Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys  
100 105 110  
Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys  
115 120 125  
Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu  
130 135 140  
Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly  
145 150 155 160  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys  
165 170 175  
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro  
180 185 190  
Ile Val

<210> 23  
<211> 1128  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1)...(1128)

<400> 23  
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1 5 10 15  
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60

AI  
com.T



61  
~~17/102~~

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca	240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser	
65 70 75 80	
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
85 90 95	
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag	336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala	
180 185 190	
atg gta aat aat tca ggg aaa gat ggg aat aca tct gca aat tct gct	624
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala	
195 200 205	
gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att	672
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile	
210 215 220	
aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg	720
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu	
225 230 235 240	
ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata aaa	768
Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys	
245 250 255	
aac gat gtt agt tta gat aat gag gca gat cac aac gga tca tta ata	816
Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile	
260 265 270	
tca gga gca tat tta att tca aac tta ata aca aaa aaa ata agt gca	864
Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala	
275 280 285	
ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct aag aaa	912
Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys	
290 295 300	

Al  
 comit

62  
18/102

tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca gat ctt 960  
 Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu 320  
 305 310 315  
 ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att tta aaa 1008  
 Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys 335  
 325 330  
 aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag tta ttt 1056  
 Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe 350  
 340 345  
 gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt act aat 1104  
 Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn 365  
 355 360  
 tca gtt aaa gag ctt aca agc taa 1128  
 Ser Val Lys Glu Leu Thr Ser \*  
 370 375

<210> 24  
 <211> 375  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<400> 24  
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
 1 5 10 15  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 20 25 30  
 Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala  
 35 40 45  
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
 50 55 60  
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser  
 65 70 75 80  
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
 85 90 95  
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
 100 105 110  
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
 115 120 125  
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
 130 135 140  
 Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
 145 150 155 160  
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
 165 170 175  
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala  
 180 185 190  
 Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala  
 195 200 205  
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile  
 210 215 220

AI  
Cm't

63  
19/102

Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu  
225 230 235 240  
Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys  
245 250 255  
Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile  
260 265 270  
Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala  
275 280 285  
Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys  
290 295 300  
Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu  
305 310 315 320  
Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys  
325 330 335  
Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe  
340 345 350  
Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn  
355 360 365  
Ser Val Lys Glu Leu Thr Ser  
370 375

<210> 25  
<211> 1124  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1)...(1124)

<400> 25  
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60  
ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser  
65 70 75 80  
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95

AI  
Cm.t

64  
207102

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140

aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala  
180 185 190

atg gta aat aat tca gga aaa gat ggg aat aca tct gca aat tct gct 624  
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala  
195 200 205

gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att 672  
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile  
210 215 220

aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg 720  
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu  
225 230 235 240

ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa aaa ata 768  
Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile  
245 250 255

caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg 816  
Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu  
260 265 270

tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa tta gat 864  
Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp  
275 280 285

gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat gct aag 912  
Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys  
290 295 300

aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat gcg caa 960  
Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln  
305 310 315 320

ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct att tta 1008  
Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
325 330 335

A1  
cm.7

65  
-21/102

ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa aag cta	1056
Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu	
340 345 350	
ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg ctt gct	1104
Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala	
355 360 365	
aat tca gtt aaa gag ctt ac	1124
Asn Ser Val Lys Glu Leu	
370	

<210> 26  
<211> 374  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 26

Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys	
50 55 60	
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser	
65 70 75 80	
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
85 90 95	
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala	
180 185 190	
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala	
195 200 205	
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile	
210 215 220	
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu	
225 230 235 240	
Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile	
245 250 255	
Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu	
260 265 270	
Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp	
275 280 285	

AI  
Cm't

66  
22/102

Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys  
290 295 300  
Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln  
305 310 315 320  
Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
325 330 335  
Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu  
340 345 350  
Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala  
355 360 365  
Asn Ser Val Lys Glu Leu  
370

<210> 27  
<211> 1137  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1)...(1137)

<400> 27  
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
20 25 30  
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60  
ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
65 70 75 80  
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125

AI  
Cm.t

67  
23/102

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys	
180 185 190	
aaa cct tcc atg gta aat aat tca ggg aaa gat ggg aat aca tct gca	624
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala	
195 200 205	
aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt	672
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser	
210 215 220	
aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt	720
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val	
225 230 235 240	
gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa	768
Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys	
245 250 255	
aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga	816
Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly	
260 265 270	
tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa	864
Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys	
275 280 285	
ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag	912
Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys	
290 295 300	
gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac	960
Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His	
305 310 315 320	
aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc	1008
Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala	
325 330 335	
att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa	1056
Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu	
340 345 350	
aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg	1104
Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met	
355 360 365	

Al  
Cm.t

68  
24/102

ctt act aat tca gtt aaa gag ctt aca agc taa  
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser \*  
370 375

1137

<210> 28  
<211> 378  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 28  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
65 70 75 80  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140  
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Leu Gly Lys Leu  
145 150 155 160  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
180 185 190  
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala  
195 200 205  
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser  
210 215 220  
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val  
225 230 235 240  
Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys  
245 250 255  
Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly  
260 265 270  
Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys  
275 280 285  
Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys  
290 295 300  
Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His  
305 310 315 320  
Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala  
325 330 335  
Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu  
340 345 350

AI  
cm.t



69  
25/102

Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met  
355 360 365  
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
370 375

<210> 29  
<211> 1133  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1)...(1133)

<400> 29  
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
20 25 30  
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60  
ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
65 70 75 80  
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125  
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140  
aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160

AI  
omit

70  
26/102

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys	
180 185 190	
aaa cct tcc atg gta aat aat tca gga aaa gat ggg aat aca tct gca	624
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala	
195 200 205	
aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt	672
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser	
210 215 220	
aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att	720
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile	
225 230 235 240	
gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt	768
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly	
245 250 255	
aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat	816
Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn	
260 265 270	
gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa	864
Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln	
275 280 285	
aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa	912
Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu	
290 295 300	
aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa	960
Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu	
305 310 315 320	
cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa	1008
His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys	
325 330 335	
gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt	1056
Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu	
340 345 350	
gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag	1104
Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu	
355 360 365	
atg ctt gct aat tca gtt aaa gag ctt ac	1133
Met Leu Ala Asn Ser Val Lys Glu Leu	
370 375	

<210> 30  
<211> 377

AI  
comit

7/  
27/102

<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 30  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
65 70 75 80  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140  
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
180 185 190  
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala  
195 200 205  
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser  
210 215 220  
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile  
225 230 235 240  
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly  
245 250 255  
Lys Lys Ile Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn  
260 265 270  
Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln  
275 280 285  
Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu  
290 295 300  
Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu  
305 310 315 320  
His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys  
325 330 335  
Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu  
340 345 350  
Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu  
355 360 365  
Met Leu Ala Asn Ser Val Lys Glu Leu  
370 375

<210> 31  
<211> 1112

AI  
cm.t

<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1)...(1112)

<400> 31

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct	48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata	192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile	
50 55 60	
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg	240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu	
65 70 75 80	
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt	288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser	
85 90 95	
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag	336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys	
100 105 110	
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag	384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln	
115 120 125	
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta	432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu	
130 135 140	
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag	480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys	
145 150 155 160	
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt	528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu	
165 170 175	
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat	576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn	
180 185 190	

AI  
Cm.t

tca aga aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt 624  
 Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val  
 195 200 205

aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac 672  
 Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn  
 210 215 220

gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata 720  
 Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile  
 225 230 235 240

gat gaa ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt 768  
 Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly  
 245 250 255

tta gag gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat 816  
 Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr  
 260 265 270

gca ata tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa 864  
 Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu  
 275 280 285

gaa tta aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt 912  
 Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe  
 290 295 300

act aat aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt 960  
 Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu  
 305 310 315 320

act gat gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa 1008  
 Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys  
 325 330 335

gat aag ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac 1056  
 Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn  
 340 345 350

tta tca aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt 1104  
 Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu  
 355 360 365

aca agt cc 1112  
 Thr Ser  
 370

&lt;210&gt; 32

&lt;211&gt; 370

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; OspC Chimera

&lt;400&gt; 32

AI  
omit

74  
~~20/102~~

Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
 1 5 10 15  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 20 25 30  
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
 35 40 45  
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
 50 55 60  
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
 65 70 75 80  
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
 85 90 95  
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys  
 100 105 110  
 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
 115 120 125  
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
 130 135 140  
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
 145 150 155 160  
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
 165 170 175  
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
 180 185 190  
 Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val  
 195 200 205  
 Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn  
 210 215 220  
 Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile  
 225 230 235 240  
 Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly  
 245 250 255  
 Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr  
 260 265 270  
 Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu  
 275 280 285  
 Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe  
 290 295 300  
 Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu  
 305 310 315 320  
 Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys  
 325 330 335  
 Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn  
 340 345 350  
 Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu  
 355 360 365  
 Thr Ser  
 370

<210> 33  
 <211> 1113  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

AI  
 unit

75  
~~31/102~~

<221> CDS  
 <222> (1)...(1113)

<400> 33

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct	48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata	192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile	
50 55 60	
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg	240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu	
65 70 75 80	
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt	288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser	
85 90 95	
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag	336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys	
100 105 110	
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag	384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln	
115 120 125	
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta	432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu	
130 135 140	
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag	480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys	
145 150 155 160	
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt	528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu	
165 170 175	
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat	576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn	
180 185 190	
tca ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt	624
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val	
195 200 205	
aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac	672
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn	
210 215 220	

AI  
 cm it

gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata	720
Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile	
225 230 235 240	
gat gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt	768
Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser	
245 250 255	
tta gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat	816
Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr	
260 265 270	
tta att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca	864
Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser	
275 280 285	
gga gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa	912
Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu	
290 295 300	
ttt act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc	960
Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly	
305 310 315 320	
gtt act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat	1008
Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp	
325 330 335	
aaa act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa	1056
Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys	
340 345 350	
aac ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag	1104
Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu	
355 360 365	
ctt aca agc	1113
Leu Thr Ser	
370	

<210> 34  
 <211> 371  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<400> 34  
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 1 5 10 15  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 20 25 30  
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
 35 40 45  
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
 50 55 60

AI  
 cm.t



Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
 65 70 75 80  
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
 85 90 95  
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys  
 100 105 110  
 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
 115 120 125  
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
 130 135 140  
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
 145 150 155 160  
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
 165 170 175  
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
 180 185 190  
 Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val  
 195 200 205  
 Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn  
 210 215 220  
 Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile  
 225 230 235 240  
 Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser  
 245 250 255  
 Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr  
 260 265 270  
 Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser  
 275 280 285  
 Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu  
 290 295 300  
 Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly  
 305 310 315 320  
 Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp  
 325 330 335  
 Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys  
 340 345 350  
 Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu  
 355 360 365  
 Leu Thr Ser  
 370

&lt;210&gt; 35

&lt;211&gt; 1112

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; OspC Chimera

&lt;221&gt; CDS

&lt;222&gt; (1)...(1112)

&lt;400&gt; 35

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 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
 1 5 10 15

48

78  
34/102

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata	192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile	
50 55 60	
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg	240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu	
65 70 75 80	
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt	288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser	
85 90 95	
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag	336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys	
100 105 110	
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag	384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln	
115 120 125	
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta	432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu	
130 135 140	
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag	480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys	
145 150 155 160	
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt	528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu	
165 170 175	
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat	576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn	
180 185 190	
tca gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt	624
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val	
195 200 205	
aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac	672
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn	
210 215 220	
gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata	720
Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile	
225 230 235 240	
gat gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt	768
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly	
245 250 255	

AI  
omit

79  
35/102

ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct 816  
Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala  
260 265 270

tat aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat 864  
Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn  
275 280 285

tca gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa 912  
Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu  
290 295 300

gat ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa 960  
Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu  
305 310 315 320

aat gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca 1008  
Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala  
325 330 335

gct aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta 1056  
Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val  
340 345 350

gaa aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa 1104  
Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys  
355 360 365

gag ctt ac 1112  
Glu Leu  
370

<210> 36  
<211> 370  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 36  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125

Al  
Cm.it

80  
26/102

Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165 170 175  
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
180 185 190  
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val  
195 200 205  
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn  
210 215 220  
Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile  
225 230 235 240  
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly  
245 250 255  
Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala  
260 265 270  
Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn  
275 280 285  
Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu  
290 295 300  
Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu  
305 310 315 320  
Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala  
325 330 335  
Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val  
340 345 350  
Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys  
355 360 365  
Glu Leu  
370

<210> 37  
<211> 1106  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1)...(1106)

<400> 37  
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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser  
1 5 10 15  
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144  
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45

AI  
cm.t

81  
37/102

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa	192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys	
50 55 60	
ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg	240
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu	
65 70 75 80	
tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat	288
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn	
85 90 95	
gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa	336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln	
100 105 110	
tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt	384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu	
115 120 125	
ggg ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa	432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys	
130 135 140	
aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt	480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe	
145 150 155 160	
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat	528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn	
165 170 175	
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca aga	576
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg	
180 185 190	
aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg	624
Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly	
195 200 205	
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt	672
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val	
210 215 220	
ggt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa	720
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu	
225 230 235 240	
ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag	768
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu	
245 250 255	
gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata	816
Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile	
260 265 270	
tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta	864
Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu	
275 280 285	

AI  
com.t

aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn 290 295 300	912
aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp 305 310 315 320	960
gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys 325 330 335	1008
ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser 340 345 350	1056
aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser 355 360 365	1104
cc	1106

AI  
cm.t

<210> 38  
<211> 368  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 38

Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser 1 5 10 15 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 20 25 30 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr 35 40 45 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys 50 55 60 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu 65 70 75 80 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn 85 90 95 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln 100 105 110 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu 115 120 125 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys 130 135 140 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe 145 150 155 160 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn 165 170 175 Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg 180 185 190 Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly 195 200 205	
--	--

Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val
210						215					220				
Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu
225					230					235					240
Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gly	Asn	Asn	Gly	Leu	Glu
			245						250					255	
Ala	Asn	Gln	Ser	Lys	Asn	Thr	Ser	Leu	Leu	Ser	Gly	Ala	Tyr	Ala	Ile
		260						265					270		
Ser	Asp	Leu	Ile	Ala	Glu	Lys	Leu	Asn	Val	Leu	Lys	Asn	Glu	Glu	Leu
	275						280					285			
Lys	Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln	Cys	Ser	Thr	Glu	Phe	Thr	Asn
	290					295					300				
Lys	Leu	Lys	Ser	Glu	His	Ala	Val	Leu	Gly	Leu	Asp	Asn	Leu	Thr	Asp
305					310					315					320
Asp	Asn	Ala	Gln	Arg	Ala	Ile	Leu	Lys	Lys	His	Ala	Asn	Lys	Asp	Lys
			325						330					335	
Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala	Val	Glu	Asn	Leu	Ser
			340					345					350		
Lys	Ala	Ala	Gln	Asp	Thr	Leu	Lys	Asn	Ala	Val	Lys	Glu	Leu	Thr	Ser
		355					360					365			

AI  
 com.t

<210> 39  
 <211> 1107  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> OSpC Chimera

<221> CDS  
 <222> (1)...(1107)

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1 5 10 15	
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc	144
Ile Thr Glu Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Thr	
35 40 45	
tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa	192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys	
50 55 60	
ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg	240
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu	
65 70 75 80	
tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat	288
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn	
85 90 95	

84  
40/102

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa	336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln	
100 105 110	
tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt	384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu	
115 120 125	
ggc ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa	432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys	
130 135 140	
aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt	480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe	
145 150 155 160	
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat	528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn	
165 170 175	
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca ggg	576
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly	
180 185 190	
aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg	624
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly	
195 200 205	
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt	672
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val	
210 215 220	
ggt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag	720
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu	
225 230 235 240	
ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat	768
Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp	
245 250 255	
aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta att	816
Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile	
260 265 270	
tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa	864
Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu	
275 280 285	
ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act	912
Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr	
290 295 300	
gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act	960
Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr	
305 310 315 320	
gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act	1008
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr	
325 330 335	

AI  
Em.t



85  
41/102

aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg 1056  
Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu  
340 345 350

tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca 1104  
Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr  
355 360 365

agc  
Ser

1107

<210> 40  
<211> 369  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 40  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45  
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
65 70 75 80  
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
85 90 95  
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
100 105 110  
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
115 120 125  
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
130 135 140  
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
145 150 155 160  
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
165 170 175  
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly  
180 185 190  
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly  
195 200 205  
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val  
210 215 220  
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu  
225 230 235 240  
Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp  
245 250 255  
Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile  
260 265 270  
Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu  
275 280 285

AI  
Commit

86  
42/102

Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr  
 290 295 300  
 Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr  
 305 310 315 320  
 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr  
 325 330 335  
 Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu  
 340 345 350  
 Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr  
 355 360 365  
 Ser

<210> 41  
 <211> 1106  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<221> CDS  
 <222> (1)...(1106)

<400> 41  
 atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48  
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser  
 1 5 10 15  
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 20 25 30  
 att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144  
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
 35 40 45  
 tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192  
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
 50 55 60  
 ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240  
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
 65 70 75 80  
 tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288  
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
 85 90 95  
 gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336  
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
 100 105 110  
 tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384  
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
 115 120 125

87  
43/102

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa	432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys	
130 135 140	
aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt	480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe	
145 150 155 160	
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat	528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn	
165 170 175	
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca gga	576
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly	
180 185 190	
aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg	624
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly	
195 200 205	
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt	672
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val	
210 215 220	
ggt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa	720
Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu	
225 230 235 240	
ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta	768
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu	
245 250 255	
gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca	816
Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr	
260 265 270	
ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa	864
Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu	
275 280 285	
aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt	912
Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe	
290 295 300	
act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt	960
Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val	
305 310 315 320	
act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa	1008
Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys	
325 330 335	
gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac	1056
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn	
340 345 350	
ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt	1104
Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu	
355 360 365	

Al  
cont

ac

<210> 42  
<211> 368  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 42  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45  
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
65 70 75 80  
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
85 90 95  
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
100 105 110  
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
115 120 125  
Gly Leu Asp Asn Leu Thr Asp Asn Ala Gln Arg Ala Ile Leu Lys  
130 135 140  
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
145 150 155 160  
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
165 170 175  
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly  
180 185 190  
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly  
195 200 205  
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val  
210 215 220  
Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu  
225 230 235 240  
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu  
245 250 255  
Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr  
260 265 270  
Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu  
275 280 285  
Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe  
290 295 300  
Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val  
305 310 315 320  
Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys  
325 330 335  
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn  
340 345 350  
Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
355 360 365

AI  
cm.t

<210> 43  
<211> 633  
<212> DNA  
<213> Borrelia burgdorferi

<220>  
<221> CDS  
<222> (1)...(633)

<400> 43  
atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt 48  
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
1 5 10 15

ata tct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 96  
Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
20 25 30

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 144  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
35 40 45

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 192  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
50 55 60

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 240  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
65 70 75 80

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 288  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
85 90 95

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 336  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
100 105 110

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 384  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
115 120 125

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 432  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
130 135 140

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 480  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
145 150 155 160

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 528  
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
165 170 175

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 576  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
180 185 190

AI  
Cm.t

90  
46/102

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa 624  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
195 200 205

aaa cct taa  
Lys Pro \*  
210

633

<210> 44  
<211> 210  
<212> PRT  
<213> Borrelia burgdorferi

<400> 44  
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
1 5 10 15  
Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
20 25 30  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
35 40 45  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
50 55 60  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
65 70 75 80  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
85 90 95  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
100 105 110  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
115 120 125  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
130 135 140  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
145 150 155 160  
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
165 170 175  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
180 185 190  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
195 200 205  
Lys Pro  
210

<210> 45  
<211> 580  
<212> DNA  
<213> Borrelia burgdorferi

<220>  
<221> CDS  
<222> (1)...(580)

<400> 45  
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15

91  
47/102

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca tcc 576  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser  
180 185 190

atg g 580  
Met

<210> 46  
<211> 193  
<212> PRT  
<213> Borrelia burgdorferi

<400> 46  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
20 25 30

AI  
Com't

92  
48/102

Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
65 70 75 80  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140  
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser  
180 185 190  
Met

AI  
com.t

<210> 47  
<211> 639  
<212> DNA  
<213> Borrelia garinii

<220>  
<221> CDS  
<222> (1)...(639)

<400> 47  
atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt 48  
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
1 5 10 15  
ata tct tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat 96  
Ile Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn  
20 25 30  
cct gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa 144  
Pro Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
35 40 45  
aaa att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag 192  
Lys Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu  
50 55 60  
act ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa 240  
Thr Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln  
65 70 75 80  
aaa ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga 288  
Lys Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly  
85 90 95



93  
49/102

tcg ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa 336  
Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys  
100 105 110

ttg agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag 384  
Leu Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys  
115 120 125

gct aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat 432  
Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His  
130 135 140

gca gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct 480  
Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala  
145 150 155 160

att tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa 528  
Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys  
165 170 175

gat tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca 576  
Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala  
180 185 190

cta act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt 624  
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser  
195 200 205

cca aaa aaa cct taa 639  
Pro Lys Lys Pro \*

<210> 48  
<211> 212  
<212> PRT  
<213> Borrelia garinii

<400> 48  
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
1 5 10 15  
Ile Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn  
20 25 30  
Pro Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
35 40 45  
Lys Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu  
50 55 60  
Thr Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln  
65 70 75 80  
Lys Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly  
85 90 95  
Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys  
100 105 110  
Leu Ser Lys Leu Lys Asn Leu Glu Leu Lys Thr Glu Ile Ala Lys  
115 120 125  
Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His  
130 135 140  
Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala  
145 150 155 160

AI  
Cm.t

94  
50/102

Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys  
165 170 175  
Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala  
180 185 190  
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser  
195 200 205  
Pro Lys Lys Pro  
210

<210> 49  
<211> 624  
<212> DNA  
<213> Borrelia afzelii

<220>  
<221> CDS  
<222> (1)...(624)

<400> 49  
atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt 48  
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
1 5 10 15  
ata tct tgt aat aat tca ggt ggg gat tct gca tct act aat cct gat 96  
Ile Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp  
20 25 30  
gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa att aca 144  
Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr  
35 40 45  
gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt 192  
Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu  
50 55 60  
tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat 240  
Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn  
65 70 75 80  
gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg ata gca 288  
Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala  
85 90 95  
gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt gta ttg 336  
Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu  
100 105 110  
aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat tgt tcc 384  
Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser  
115 120 125  
caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt ggt ata 432  
Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile  
130 135 140  
caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa aca cat 480  
Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His  
145 150 155 160

AI  
Cm.T

95  
51/102

gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca 528  
Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser  
165 170 175

cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat tca gtt 576  
Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val  
180 185 190

aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 624  
Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro \*  
195 200 205

<210> 50  
<211> 207  
<212> PRT  
<213> Borrelia afzelii

<400> 50  
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
1 5 10 15  
Ile Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp  
20 25 30  
Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr  
35 40 45  
Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu  
50 55 60  
Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn  
65 70 75 80  
Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala  
85 90 95  
Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu  
100 105 110  
Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser  
115 120 125  
Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile  
130 135 140  
Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His  
145 150 155 160  
Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser  
165 170 175  
Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val  
180 185 190  
Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro  
195 200 205

<210> 51  
<211> 1680  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1680)

<400> 51

AI  
omit

96  
52/102

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct	48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa	192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys	
50 55 60	
ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca	240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser	
65 70 75 80	
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
85 90 95	
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag	336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala	
180 185 190	
atg ggt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct	624
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro	
195 200 205	
gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa	672
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
210 215 220	
att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act	720
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr	
225 230 235 240	

Al  
mit

97  
53/102

ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa	768
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys	
245 250 255	
ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg	816
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser	
260 265 270	
ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg	864
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu	
275 280 285	
agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct	912
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala	
290 295 300	
aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca	960
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala	
305 310 315 320	
gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att	1008
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile	
325 330 335	
tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat	1056
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp	
340 345 350	
tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta	1104
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu	
355 360 365	
act aat tca gtt aaa gaa ctt ggt cac cgt aat aat tca ggt ggg gat	1152
Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp	
370 375 380	
tct gca tct act aat cct gat gag tct gca aaa gga cct aat ctt acc	1200
Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr	
385 390 395 400	
gta ata agc aaa aaa att aca gat tct aat gca ttt tta ctg gct gtg	1248
Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val	
405 410 415	
aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt tct aaa gct	1296
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala	
420 425 430	
att ggt aaa aaa ata aaa aat gat ggt act tta gat aac gaa gca aat	1344
Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn	
435 440 445	
cga aac gaa tca ttg ata gca gga gct tat gaa ata tca aaa cta ata	1392
Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile	
450 455 460	

AI  
Con.T

98  
-54/102

aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag aaa aaa att 1440  
Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile  
465 470 475 480

aaa gag gct aag gat tgt tcc caa aaa ttt act act aag cta aaa gat 1488  
Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp  
485 490 495

agt cat gca gag ctt ggt ata caa agc gtt cag gat gat aat gca aaa 1536  
Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys  
500 505 510

aaa gct att tta aaa aca cat gga act aaa gac aag ggt gct aaa gaa 1584  
Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu  
515 520 525

ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa 1632  
Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln  
530 535 540

gca gca tta act aat tca gtt aaa gag ctt aca aat cct gtt gtg gca 1680  
Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala  
545 550 555 560

<210> 52  
<211> 560  
<212> PRT  
<213> ospC Chimera

<400> 52  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser  
65 70 75 80  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140  
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala  
180 185 190  
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro  
195 200 205

A1  
Cm.T

99  
55/102

Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
210 215 220  
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr  
225 230 235 240  
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys  
245 250 255  
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser  
260 265 270  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu  
275 280 285  
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala  
290 295 300  
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala  
305 310 315 320  
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile  
325 330 335  
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp  
340 345 350  
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu  
355 360 365  
Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp  
370 375 380  
Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr  
385 390 395 400  
Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val  
405 410 415  
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala  
420 425 430  
Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn  
435 440 445  
Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile  
450 455 460  
Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile  
465 470 475 480  
Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp  
485 490 495  
Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys  
500 505 510  
Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu  
515 520 525  
Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln  
530 535 540  
Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala  
545 550 555 560

<210> 53  
<211> 1137  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1137)

<400> 53  
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15

100  
56/102

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys  
100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432  
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576  
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
180 185 190

tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga 624  
Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly  
195 200 205

cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt 672  
Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe  
210 215 220

tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa 720  
Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu  
225 230 235 240

AI  
cm.t



161  
57/102

ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat 768  
Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp  
245 250 255

aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata 816  
Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile  
260 265 270

tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta 864  
Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu  
275 280 285

aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act 912  
Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr  
290 295 300

aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat 960  
Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp  
305 310 315 320

gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag 1008  
Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys  
325 330 335

ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca 1056  
Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser  
340 345 350

aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat 1104  
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn  
355 360 365

cct gtt gtg gca gaa agt cca aaa aaa cct taa 1137  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro \*

<210> 54  
<211> 378  
<212> PRT  
<213> ospC Chimera

<400> 54  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125

AI  
Cm't

162  
58/102

Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165 170 175  
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
180 185 190  
Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly  
195 200 205  
Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe  
210 215 220  
Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu  
225 230 235 240  
Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp  
245 250 255  
Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile  
260 265 270  
Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu  
275 280 285  
Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr  
290 295 300  
Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp  
305 310 315 320  
Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys  
325 330 335  
Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser  
340 345 350  
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn  
355 360 365  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro  
370 375

<210> 55  
<211> 1158  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1158)

<400> 55  
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60

103  
-59/102

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser  
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140

aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa 576  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
180 185 190

aaa cct ttc cat ggt aat aat tca ggt ggg gat tct gca tct act aat 624  
Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn  
195 200 205

cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa 672  
Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys  
210 215 220

att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct 720  
Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala  
225 230 235 240

ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata 768  
Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile  
245 250 255

aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg 816  
Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
260 265 270

ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt 864  
Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser  
275 280 285

A1  
cm.t

164  
60/102

gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat	912
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp	
290 295 300	
tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt	960
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu	
305 310 315 320	
ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa	1008
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys	
325 330 335	
aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt	1056
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe	
340 345 350	
aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat	1104
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn	
355 360 365	
tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa	1152
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys	
370 375 380	
cct taa	1158
Pro *	
385	

<210> 56  
 <211> 385  
 <212> PRT  
 <213> ospC Chimera

<400> 56

Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys	
50 55 60	
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser	
65 70 75 80	
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
85 90 95	
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys	
180 185 190	

A1  
cm.t

105  
61/102

Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn  
195 200 205  
Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys  
210 215 220  
Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala  
225 230 235 240  
Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile  
245 250 255  
Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
260 265 270  
Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser  
275 280 285  
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp  
290 295 300  
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu  
305 310 315 320  
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys  
325 330 335  
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe  
340 345 350  
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn  
355 360 365  
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys  
370 375 380  
Pro  
385

<210> 57  
<211> 1161  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1161)

<400> 57  
atg tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct 48  
Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro  
1 5 10 15  
gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa 96  
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act 144  
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45  
ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa 192  
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys  
50 55 60  
ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg 240  
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser  
65 70 75 80

AI  
cm. x

166  
62/102

ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu	
85 90 95	
agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct	336
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala	
100 105 110	
aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca	384
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala	
115 120 125	
gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att	432
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile	
130 135 140	
tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat	480
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp	
145 150 155 160	
tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta	528
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu	
165 170 175	
act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt cca	576
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro	
180 185 190	
aaa aaa cct cat atg gct aat aat tca ggt ggg gat tct gca tct act	624
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr	
195 200 205	
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa	672
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys	
210 215 220	
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag	720
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu	
225 230 235 240	
gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa	768
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys	
245 250 255	
ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca	816
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser	
260 265 270	
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta	864
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu	
275 280 285	
agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag	912
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys	
290 295 300	
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag	960
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu	
305 310 315 320	

AI  
com.t

167  
63/102

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta 1008  
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu  
325 330 335

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta 1056  
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu  
340 345 350

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act 1104  
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr  
355 360 365

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa 1152  
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys  
370 375 380

aaa cct taa 1161  
Lys Pro \*  
385

<210> 58  
<211> 386  
<212> PRT  
<213> ospC Chimera

<400> 58  
Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro  
1 5 10 15  
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45  
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys  
50 55 60  
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser  
65 70 75 80  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu  
85 90 95  
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala  
100 105 110  
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala  
115 120 125  
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile  
130 135 140  
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp  
145 150 155 160  
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu  
165 170 175  
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro  
180 185 190  
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr  
195 200 205  
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys  
210 215 220  
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu  
225 230 235 240

AI  
cm.t

108  
64/102

Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys  
245 250 255  
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser  
260 265 270  
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu  
275 280 285  
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys  
290 295 300  
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu  
305 310 315 320  
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu  
325 330 335  
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu  
340 345 350  
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr  
355 360 365  
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys  
370 375 380  
Lys Pro  
385

<210> 59  
<211> 1197  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1197)

<400> 59  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
100 105 110

A1  
cm. x



109  
~~65/102~~

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
 Lys Glu Lys Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205

cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat 672  
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
 210 215 220

ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat 720  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 225 230 235 240

ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc 768  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
 245 250 255

gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct 816  
 Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala  
 260 265 270

aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag 864  
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu  
 275 280 285

gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac 912  
 Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn  
 290 295 300

tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag 960  
 Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys  
 305 310 315 320

gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa 1008  
 Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys  
 325 330 335

Al  
 com.it

110  
66/102

tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat 1056  
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp  
340 345 350

aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc 1104  
Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly  
355 360 365

gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa 1152  
Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys  
370 375 380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc 1197  
Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
385 390 395

<210> 60  
<211> 399  
<212> PRT  
<213> ospC Chimera

<400> 60  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
65 70 75 80  
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
85 90 95  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
100 105 110  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
115 120 125  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
130 135 140  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
145 150 155 160  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
165 170 175  
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
180 185 190  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
195 200 205  
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
210 215 220  
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
225 230 235 240  
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
245 250 255  
Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala  
260 265 270

AI  
con.x

111  
67/102

Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu  
275 280 285  
Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn  
290 295 300  
Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys  
305 310 315 320  
Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys  
325 330 335  
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp  
340 345 350  
Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly  
355 360 365  
Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys  
370 375 380  
Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
385 390 395

<210> 61  
<211> 1196  
<212> DNA  
<213> ospC Chimera

AI  
Com't

<220>  
<221> CDS  
<222> (1)...(1196)

<400> 61  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
65 70 75 80  
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
85 90 95  
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
100 105 110  
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130 135 140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145 150 155 160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat	672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp	
210 215 220	
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat	720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
225 230 235 240	
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg	768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu	
245 250 255	
gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct	816
Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala	
260 265 270	
act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc	864
Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val	
275 280 285	
gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca	912
Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
290 295 300	
aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta	960
Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu	
305 310 315 320	
aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa	1008
Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys	
325 330 335	
aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat	1056
Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp	
340 345 350	

AI  
Cm.t

113  
~~69/102~~

gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag 1104  
 Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys  
 355 360 365

ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca 1152  
 Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala  
 370 375 380

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt ac 1196  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
 385 390 395

<210> 62  
 <211> 398  
 <212> PRT  
 <213> ospC Chimera

<400> 62  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
 210 215 220  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 225 230 235 240  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
 245 250 255  
 Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala  
 260 265 270  
 Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val  
 275 280 285  
 Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 290 295 300

AI  
 Cont

114  
70/102

Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu  
305 310 315 320  
Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys  
325 330 335  
Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp  
340 345 350  
Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys  
355 360 365  
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala  
370 375 380  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
385 390 395

<210> 63  
<211> 1185  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1185)

<400> 63  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432  
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140

AI  
Comit

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576  
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205

agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct 672  
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
210 215 220

gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata 720  
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
225 230 235 240

agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa 768  
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
245 250 255

gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt 816  
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly  
260 265 270

aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac 864  
Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn  
275 280 285

gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa 912  
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys  
290 295 300

aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa 960  
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu  
305 310 315 320

aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa 1008  
Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu  
325 330 335

cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa 1056  
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys  
340 345 350

gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt 1104  
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu  
355 360 365

AI  
Cont

116  
72/102

gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag 1152  
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu  
370 375 380

atg ctt act aat tca gtt aaa gag ctt aca agc 1185  
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
385 390 395

<210> 64  
<211> 395  
<212> PRT  
<213> ospC Chimera

<400> 64  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125  
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175  
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205  
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
210 215 220  
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
225 230 235 240  
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
245 250 255  
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly  
260 265 270  
Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn  
275 280 285  
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys  
290 295 300  
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu  
305 310 315 320  
Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu  
325 330 335  
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys  
340 345 350

AI  
cm.t



117  
23/10/2

Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu  
 355 360 365  
 Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu  
 370 375 380  
 Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
 385 390 395

<210> 65  
 <211> 1184  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1) ... (1184)

<400> 65  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 65 70 75 80  
 gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
 85 90 95  
 gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336  
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 100 105 110  
 acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384  
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
 115 120 125  
 aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432  
 Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
 130 135 140  
 aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480  
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
 145 150 155 160

AI  
Cm it

118  
74/102

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp 165 170 175	528
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu 180 185 190	576
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr 195 200 205	624
agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser 210 215 220	672
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile 225 230 235 240	720
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu 245 250 255	768
att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile 260 265 270	816
ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His 275 280 285	864
aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr 290 295 300	912
caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile 305 310 315 320	960
gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly 325 330 335	1008
gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys 340 345 350	1056
aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu 355 360 365	1104
ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys 370 375 380	1152
gag atg ctt gct aat tca gtt aaa gag ctt ac Glu Met Leu Ala Asn Ser Val Lys Glu Leu 385 390	1184

Al  
com.t

<210> 66  
<211> 394  
<212> PRT  
<213> ospC Chimera

<400> 66  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125  
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175  
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205  
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
210 215 220  
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
225 230 235 240  
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
245 250 255  
Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
260 265 270  
Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His  
275 280 285  
Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr  
290 295 300  
Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile  
305 310 315 320  
Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly  
325 330 335  
Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys  
340 345 350  
Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu  
355 360 365  
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys  
370 375 380  
Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
385 390

AI  
cm.t

120  
76/102

<210> 67  
<211> 1184  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1184)

<400> 67  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432  
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576  
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190

AI  
Cm.t

121  
77/102

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205

agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct 672  
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser  
210 215 220

aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata 720  
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
225 230 235 240

agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa 768  
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
245 250 255

gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att 816  
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
260 265 270

ggg aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac 864  
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn  
275 280 285

aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa 912  
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu  
290 295 300

aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca 960  
Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr  
305 310 315 320

gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat 1008  
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His  
325 330 335

gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct 1056  
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala  
340 345 350

att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa 1104  
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu  
355 360 365

aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca 1152  
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr  
370 375 380

tta aaa aat gct gtt aaa gag ctt aca agt cc 1184  
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser  
385 390

<210> 68  
<211> 394  
<212> PRT  
<213> ospC Chimera

<400> 68

AI  
cm't

122  
78/102

Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125  
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175  
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205  
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser  
210 215 220  
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
225 230 235 240  
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
245 250 255  
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
260 265 270  
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn  
275 280 285  
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu  
290 295 300  
Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr  
305 310 315 320  
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His  
325 330 335  
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala  
340 345 350  
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu  
355 360 365  
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr  
370 375 380  
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser  
385 390

AI  
Cm.it

<210> 69  
<211> 1209  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS

123  
79/102

<222> (1)...(1209)

<400> 69  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432  
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576  
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205

agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act 672  
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr  
210 215 220

AI  
omit

124  
80/102

aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa 720  
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys  
225 230 235 240

aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag 768  
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu  
245 250 255

gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa 816  
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys  
260 265 270

ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca 864  
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser  
275 280 285

ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta 912  
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu  
290 295 300

agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag 960  
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys  
305 310 315 320

gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag 1008  
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu  
325 330 335

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta 1056  
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu  
340 345 350

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta 1104  
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu  
355 360 365

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act 1152  
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr  
370 375 380

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa 1200  
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys  
385 390 395 400

aaa cct taa 1209  
Lys Pro \*

<210> 70  
<211> 402  
<212> PRT  
<213> ospC Chimera

<400> 70  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

AI  
Cm.T



125  
81/102

Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125  
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175  
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205  
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr  
210 215 220  
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys  
225 230 235 240  
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu  
245 250 255  
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys  
260 265 270  
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser  
275 280 285  
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu  
290 295 300  
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys  
305 310 315 320  
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu  
325 330 335  
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu  
340 345 350  
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu  
355 360 365  
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr  
370 375 380  
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys  
385 390 395 400  
Lys Pro

AI  
Cm.t

<210> 71  
<211> 1179  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1179)

126  
82/102

<400> 71  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240  
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288  
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336  
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384  
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
115 120 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432  
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
130 135 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480  
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
145 150 155 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528  
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
180 185 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct 624  
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
195 200 205

att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat 672  
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
210 215 220

AI  
Cmt

127  
83/102

tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
225 230 235 240	
aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa	768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu	
245 250 255	
act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa	816
Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys	
260 265 270	
ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca	864
Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser	
275 280 285	
tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata	912
Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile	
290 295 300	
agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct	960
Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala	
305 310 315 320	
aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca	1008
Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr	
325 330 335	
gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att	1056
Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile	
340 345 350	
tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag	1104
Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys	
355 360 365	
tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt	1152
Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu	
370 375 380	
act aat tca gtt aaa gag ctt aca agc	1179
Thr Asn Ser Val Lys Glu Leu Thr Ser	
385 390	

<210> 72  
 <211> 393  
 <212> PRT  
 <213> ospC Chimera

<400> 72  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
 50 55 60

AI  
Cm.t

128  
84/102

Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
65 70 75 80  
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
85 90 95  
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
100 105 110  
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
115 120 125  
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
130 135 140  
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
145 150 155 160  
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
165 170 175  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
180 185 190  
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
195 200 205  
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
210 215 220  
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
225 230 235 240  
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
245 250 255  
Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys  
260 265 270  
Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser  
275 280 285  
Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile  
290 295 300  
Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala  
305 310 315 320  
Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr  
325 330 335  
Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile  
340 345 350  
Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys  
355 360 365  
Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu  
370 375 380  
Thr Asn Ser Val Lys Glu Leu Thr Ser  
385 390

<210> 73  
<211> 1178  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1178)

<400> 73  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

AI  
cm.t

129  
85/102

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240  
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288  
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336  
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384  
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
115 120 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432  
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
130 135 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480  
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
145 150 155 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528  
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
180 185 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct 624  
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
195 200 205

att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat 672  
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
210 215 220

tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa 720  
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
225 230 235 240

aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa 768  
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu  
245 250 255

A1  
cm.t

act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa 816  
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
260 265 270

aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga 864  
Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly  
275 280 285

aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa 912  
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys  
290 295 300

tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat 960  
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn  
305 310 315 320

gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat 1008  
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His  
325 330 335

gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct 1056  
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala  
340 345 350

att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa 1104  
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu  
355 360 365

aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg 1152  
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met  
370 375 380

ctt gct aat tca gtt aaa gag ctt ac 1178  
Leu Ala Asn Ser Val Lys Glu Leu  
385 390

<210> 74  
<211> 392  
<212> PRT  
<213> ospC Chimera

<400> 74  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
50 55 60  
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
65 70 75 80  
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
85 90 95  
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
100 105 110

AI  
cm.t

131  
-87/102

Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
115 120 125  
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
130 135 140  
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
145 150 155 160  
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
165 170 175  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
180 185 190  
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
195 200 205  
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
210 215 220  
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
225 230 235 240  
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu  
245 250 255  
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
260 265 270  
Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly  
275 280 285  
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys  
290 295 300  
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn  
305 310 315 320  
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His  
325 330 335  
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala  
340 345 350  
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu  
355 360 365  
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met  
370 375 380  
Leu Ala Asn Ser Val Lys Glu Leu  
385 390

<210> 75  
<211> 1178  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1178)

<400> 75  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

AI  
Comit

132  
-88/102

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240  
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288  
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336  
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384  
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
115 120 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432  
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
130 135 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480  
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
145 150 155 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528  
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
180 185 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct 624  
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
195 200 205

att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat 672  
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn  
210 215 220

tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa 720  
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
225 230 235 240

aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag 768  
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
245 250 255

acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag 816  
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
260 265 270

AI  
cm.t



aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca 864  
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser  
275 280 285

ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta 912  
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu  
290 295 300

aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag 960  
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys  
305 310 315 320

caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg 1008  
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val  
325 330 335

ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta 1056  
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu  
340 345 350

aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta 1104  
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu  
355 360 365

ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa 1152  
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys  
370 375 380

aat gct gtt aaa gag ctt aca agt cc 1178  
Asn Ala Val Lys Glu Leu Thr Ser  
385 390

<210> 76  
<211> 392  
<212> PRT  
<213> ospC Chimera

<400> 76  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
50 55 60  
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
65 70 75 80  
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
85 90 95  
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
100 105 110  
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
115 120 125  
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
130 135 140  
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
145 150 155 160

AI  
Comit

134  
90/102

AI  
Cm't

Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
175  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
180  
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
195  
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn  
210  
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
225  
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
245  
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
260  
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser  
275  
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu  
290  
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys  
305  
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val  
325  
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu  
340  
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu  
355  
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys  
370  
Asn Ala Val Lys Glu Leu Thr Ser  
385

<210> 77  
<211> 1230  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1230)

<400> 77  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 15  
1 5 10  
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 30  
20 25  
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 45  
35 40  
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 60  
50 55

135  
91/102

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 80  
65 70 75

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 95  
85 90

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 110  
100 105

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 125  
115 120

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 140  
130 135

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 160  
145 150 155

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 175  
165 170

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576  
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 190  
180 185

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 205  
195 200

cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca 672  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser 220  
210 215

ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct 720  
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro 240  
225 230 235

aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta 768  
Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu 255  
245 250

ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt 816  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu 270  
260 265

tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac 864  
Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn 285  
275 280

gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca 912  
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser 300  
290 300

AI  
Cm.t

136  
~~92/102~~

aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag 960  
 Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys 320  
 305 310 315

aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag 1008  
 Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys 335  
 325 330

cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat 1056  
 Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp 350  
 340 345

aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt 1104  
 Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly 365  
 355 360

gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa 1152  
 Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys 380  
 370 375

gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct 1200  
 Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro 400  
 385 390 395

gtt gtg gca gaa agt cca aaa aaa cct taa 1230  
 Val Val Ala Glu Ser Pro Lys Lys Pro \*

<210> 78  
 <211> 409  
 <212> PRT  
 <213> ospC Chimera

<400> 78  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 15  
 1 5 10  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 30  
 20 25  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 45  
 35 40  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 60  
 50 55  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 80  
 65 70 75  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 95  
 85 90  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 110  
 100 105  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 125  
 115 120  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 140  
 130 135  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 160  
 145 150 155  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 175  
 165 170

AI  
 Com't

137  
93/102

AI  
Com. +

Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
180 185 190  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
195 200 205  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser  
210 215 220  
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro  
225 230 235 240  
Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu  
245 250 255  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
260 265 270  
Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn  
275 280 285  
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser  
290 295 300  
Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys  
305 310 315 320  
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys  
325 330 335  
Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp  
340 345 350  
Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly  
355 360 365  
Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys  
370 375 380  
Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro  
385 390 395 400  
Val Val Ala Glu Ser Pro Lys Lys Pro  
405

<210> 79  
<211> 1209  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1209)

<400> 79  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys 15  
1 5 10  
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 30  
20 25  
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 45  
35 40  
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 60  
50 55

138  
~~347102~~

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 80  
65 70 75

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 95  
85 90

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 110  
100 105

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
Ser Thr Leu Ile Lys Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 125  
115 120

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 140  
130 135

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 160  
145 150 155

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 175  
165 170

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576  
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 190  
180 185

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 205  
195 200

cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca 672  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser 220  
210 215

ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa 720  
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys 240  
225 230 235

ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca 768  
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala 255  
245 250

gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat 816  
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp 270  
260 265

gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta 864  
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu 285  
275 280

gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta 912  
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu 300  
290 295

AI  
Cm.t

139  
95/102

att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga 960  
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly 320  
305 310 315

gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt 1008  
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe 335  
325 330

act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt 1056  
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val 350  
340 345

act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa 1104  
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys 365  
355 360

act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac 1152  
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn 380  
370 375

ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt 1200  
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu 400  
385 390 395

aca agc taa 1209  
Thr Ser \*

AI  
Cm't

<210> 80  
<211> 402  
<212> PRT  
<213> ospC Chimera

<400> 80  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 15  
1 5 10  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 30  
20 25  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 45  
35 40  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 60  
50 55  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 80  
65 70 75  
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 95  
85 90  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 110  
100 105  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 125  
115 120  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 140  
130 135  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 160  
145 150 155  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 175  
165 170

140  
96/102

Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
180 185 190  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
195 200 205  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser  
210 215 220  
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
225 230 235 240  
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala  
245 250 255  
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp  
260 265 270  
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu  
275 280 285  
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu  
290 295 300  
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly  
305 310 315 320  
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe  
325 330 335  
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val  
340 345 350  
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys  
355 360 365  
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn  
370 375 380  
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu  
385 390 395 400  
Thr Ser

AI  
Cm't

<210> 81  
<211> 1205  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1205)

<400> 81  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 15  
1 5 10  
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 30  
20 25  
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 45  
35 40  
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 60  
50



141  
97/102

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 80  
65 70 75

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 95  
85 90

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 110  
100 105

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 125  
115 120

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
Lys Glu Lys Ile Asp Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 140  
130 135

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 160  
145 150 155

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 175  
165 170

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576  
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 190  
180 185

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 205  
195 200

cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca 672  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser 220  
210 215

gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa 720  
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys 240  
225 230 235

ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca 768  
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala 255  
245 250

gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat 816  
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp 270  
260 265

gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt 864  
Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly 285  
275 280

tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat 912  
Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr 300  
290 295

AI  
Cm.it

142  
98/102

aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca 960  
Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser 320  
305 310 315

gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat 1008  
Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp 335  
325 330

ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat 1056  
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn 350  
340 345

gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct 1104  
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala 365  
355 360

aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa 1152  
Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu 380  
370 375

aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag 1200  
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu 400  
385 390 395

ctt ac 1205  
Leu

<210> 82  
<211> 401  
<212> PRT  
<213> ospC Chimera

<400> 82  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 15  
1 5 10  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 30  
20 25  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 45  
35 40  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 60  
50 55  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 80  
65 70 75  
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 95  
85 90  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 110  
100 105  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 125  
115 120  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 140  
130 135  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 160  
145 150 155  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 175  
165 170  
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser

AI  
Cm't

143  
~~99/102~~

Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 180  
 195  
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser 200  
 210  
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys 215  
 225  
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala 230  
 245  
 Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp 250  
 260  
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly 265  
 275  
 Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr 280  
 290  
 Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser 295  
 305  
 Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp 310  
 325  
 Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn 315  
 340  
 Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala 330  
 355  
 Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu 335  
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 Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu 345  
 385  
 Leu 360  
 375  
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 395  
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<210> 83  
 <211> 1236  
 <212> DNA  
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 <221> CDS  
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<400> 83  
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 15  
 1  
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gta ctt gct gtt aaa gaa gtt gag act ttg gtt tta tct ata gat gaa 240  
Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu 80  
65 70 75

ctt gct aag aaa gct att ggt caa aaa ata gac aat aat aat ggt tta 288  
Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu 95  
85 90

gct gct tta aat aat cag aat gga tct ttg tta gca gga gcc tat gca 336  
Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala 110  
100 105

ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa 384  
Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu 125  
115 120

gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt 432  
Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe 140  
130 135

act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct 480  
Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala 160  
145 150 155

acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc 528  
Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr 175  
165 170

gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt 576  
Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly 190  
180 185

ttg tta aaa gca gct caa gta gca cta act aat tca gtt aaa gaa ctt 624  
Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu 205  
195 200

aca agt cct gtt gta gca gaa agt cca aaa aaa cct cat atg gct aat 672  
Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn 220  
210 215

aat tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa 720  
Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys 240  
225 230 235

gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca 768  
Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala 255  
245 250

ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat 816  
Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp 270  
260 265

gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta 864  
Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu 285  
275 280

gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa 912  
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu 300  
290 295

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ata tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa 960  
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu 320  
305 310 315

tta aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act 1008  
Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr 335  
325 330

act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag 1056  
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln 350  
340 345

gat gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac 1104  
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp 365  
355 360

aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg 1152  
Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu 380  
370 375

tca aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca 1200  
Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr 400  
385 390 395

aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 1236  
Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro \* 410  
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Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys 30  
20 25  
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly 45  
35 40  
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe 60  
50 55  
Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu 80  
65 70 75  
Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu 95  
85 90  
Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala 110  
100 105  
Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu 125  
115 120  
Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe 140  
130 135  
Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala 160  
145 150 155  
Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr 175  
165 170

Al  
Cm't

146  
102/102

Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly  
180 185 190  
Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu  
195 200 205  
Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn  
210 215 220  
Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys  
225 230 235 240  
Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala  
245 250 255  
Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp  
260 265 270  
Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu  
275 280 285  
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu  
290 295 300  
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu  
305 310 315 320  
Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr  
325 330 335  
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln  
340 345 350  
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp  
355 360 365  
Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu  
370 375 380  
Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr  
385 390 395 400  
Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro  
405 410

AI  
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